

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Hitz, William D.
Thorpe, Catherine J.
Tingey, Scott V.

<120> PHYTIC ACID BIOSYNTHETIC ENZYMES

<130> BB1165 US NA

<140> 09/686,522

<141> 2000-10-11

<150> 60/082,960

<151> 1998-04-24

<150> PCT/US99/08790

<151> 1999-04-22

<160> 24

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<210> 1

<211> 462

<212> DNA

<213> Oryza sativa

<400> 1

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accacaagtt catcggcgag gagacgtccg cggggctcgg cgccaccgcg gacctcaccg 360
acgaccgcac ctggatcgtc gacccctcgc atggcaccac caatttcgtc catggcttcc 420
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<210> 2

<211> 114

<212> PRT

<213> Oryza sativa

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Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr Lys Asn Val Glu
      20              25              30
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```
His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
      35              40              45
```

```
Asp Leu Ile Phe Asn His Leu Arg Lys His Tyr Pro Asp His Lys Phe
      50              55              60
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```
Ile Gly Glu Glu Thr Ser Ala Gly Leu Gly Ala Thr Ala Asp Leu Thr
      65              70              75              80
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Asp Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
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Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Val Gly
100 105 110

Lys Ile
114

<210> 3
<211> 561
<212> DNA
<213> Glycine max

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<223> n = a, c, g or t

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tcctcgcatc tgcggtcgac gcggctcaga aagctggcga gattattcga aaaggcttct 180
accagaccaa aaatgtggaa cacaaaggac aggttgattt ggtcacagaa actgataaag 240
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tgatccctgg atggaactac taacttgtgc atgggttccc tttgtttgtg tcccattggc 420
tcacaattgg aaaaatctac aattggtgtt gtatacaatc aatataatga cttttctgga 480
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ctncantgag gngganaaaa c 561

<210> 4
<211> 168
<212> PRT
<213> Glycine max

<400> 4
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Ala Ala Gln Lys Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr
 20 25 30
 Lys Asn Val Glu His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp
 35 40 45
 Lys Ala Cys Glu Glu Leu Ile Phe Asn His Leu Lys Gln Leu Tyr Pro
 50 55 60
 Thr His Lys Phe Ile Gly Glu Glu Thr Thr Ala Ala Tyr Gly Thr Thr
 65 70 75 80
 Glu Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr
 85 90 95
 Thr Asn Phe Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu
 100 105 110
 Thr Ile Gly Lys Thr Pro Thr Ile Gly Val Val Tyr Asn Pro Ile Ile
 115 120 125
 Asn Glu Leu Phe Thr Gly Ile His Gly Lys Gly Ala Phe Leu Asn Gly
 130 135 140
 Asn Pro Ile Lys Val Ser Ser Gln Thr Glu Leu Ile Ser Ser Leu Leu
 145 150 155 160
 Ala Thr Glu Ala Gly Thr Lys Arg
 165

<210> 5
 <211> 667
 <212> DNA
 <213> Glycine max

<400> 5
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 cagattttgc aataacatct cagcgagtag cagtttcaaa ccctttctaa aaggatgaac 180
 ttgtggaaac tcggcgcaaa atgggggtggg aaattttacaa ttaaccattg gcaagacctt 240
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 aagttttacg tagaagttcc aggttaaaaa gggttttagaa ttttaacttc ctccgggggc 360
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 aaaaaactcc ctaaacaatgg gaagaagcac ctccacaggg cacgcgttcc caaacctggt 480
 cggaaggcc gtgggcattc gggaaaccgg taccaatcaa ggatcctccc ggaacccaaa 540
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 ggggccg 667

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 <211> 73
 <212> PRT
 <213> Glycine max

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 <221> UNSURE
 <222> (56)
 <223> Xaa = any amino acid
 <400> 6

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 1 5 10 15
 Pro Trp Asp Val Ala Gly Gly Ala Val Ile Val Arg Glu Ala Gly Gly
 20 25 30
 Val Val Phe Asp Pro Ser Gly Ala Asp Phe Ala Ile Thr Ser Gln Arg
 35 40 45
 Val Ala Val Ser Asn Pro Phe Xaa Lys Asp Glu Leu Val Glu Thr Arg
 50 55 60
 Arg Lys Met Gly Trp Glu Ile Tyr Asn
 65 70

<210> 7
 <211> 1003
 <212> DNA
 <213> Triticum aestivum

<400> 7
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 ccaagagcgc cggcgagatt atccgcaaga gcttttacct aagcaagaaa gtggagcaca 120
 agggccaggt ggatttggtg acggagacgg acaaggcatg cgaggatctc atcttcaacc 180
 acctccgat gctctacccg gaccacaagt tcatcggcga ggagacgtct gcagccctcg 240
 gctccaccga tgacctcacc tacgacccca cctggatagt cgacccctc gatggcacca 300
 ccaacttcgt tcatggcctt ccttttggtg gcgtctcgat tggcctcacc attgggaaga 360
 tccccaccgt tggagttgtg tacaacccca tcatgaatga gcttttcaca gctgttcgtg 420
 gaaaaggtgc ttttctcaat ggctctccaa ttaaaacatc gcctcaaaat gagttggtga 480
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 ccaacagaat taataagtta ctattcaaga ttagatctat acgtatgtgt ggctcttttg 600
 ctctaaacat gtgtggagtt gcttgtggta ggctagattt gtgttatgag atcggttttg 660
 gtggccctg ggatgtggct gctggagctt tgattctaaa ggaagctggg ggttttggtt 720
 ttgatccgag cggatgatgag tttgatctga tggcgcaaag aatggcagga tcaaattggc 780
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 ttcaagtaga atgaaagaat gtaagatggc cccaccaata agtaattgag ggctactttt 900
 tgtgtagttc tatatgcata ttttgcaaac gtggcggatg taatgacatt ggatatattg 960
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<210> 8
 <211> 267
 <212> PRT
 <213> Triticum aestivum

<400> 8
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 Ala Gly Glu Ile Ile Arg Lys Ser Phe Tyr Leu Ser Lys Lys Val Glu
 20 25 30
 His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
 35 40 45
 Asp Leu Ile Phe Asn His Leu Arg Met Leu Tyr Pro Asp His Lys Phe
 50 55 60
 Ile Gly Glu Glu Thr Ser Ala Ala Leu Gly Ser Thr Asp Asp Leu Thr
 65 70 75 80

Tyr Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
 85 90 95
 Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Ile Gly
 100 105 110
 Lys Ile Pro Thr Val Gly Val Val Tyr Asn Pro Ile Met Asn Glu Leu
 115 120 125
 Phe Thr Ala Val Arg Gly Lys Gly Ala Phe Leu Asn Gly Ser Pro Ile
 130 135 140
 Lys Thr Ser Pro Gln Asn Glu Leu Val Lys Ala Leu Met Val Thr Glu
 145 150 155 160
 Val Gly Thr Lys Arg Asp Lys Ser Thr Leu Asp Asp Thr Thr Asn Arg
 165 170 175
 Ile Asn Lys Leu Leu Phe Lys Ile Arg Ser Ile Arg Met Cys Gly Ser
 180 185 190
 Leu Ala Leu Asn Met Cys Gly Val Ala Cys Gly Arg Leu Asp Leu Cys
 195 200 205
 Tyr Glu Ile Gly Phe Gly Gly Pro Trp Asp Val Ala Ala Gly Ala Leu
 210 215 220
 Ile Leu Lys Glu Ala Gly Gly Phe Val Phe Asp Pro Ser Gly Asp Glu
 225 230 235 240
 Phe Asp Leu Met Ala Gln Arg Met Ala Gly Ser Asn Gly His Leu Lys
 245 250 255
 Asp Gln Phe Ile Lys Ala Leu Gly Asp Ala Ser
 260 265

<210> 9
 <211> 1090
 <212> DNA
 <213> Hordeum vulgare

<400> 9
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 ccacatcata cttggggagg aaggtggcct tattggagat tctttgtcag agtatctctg 120
 gtgcattgat ccttttagatg gaacaacaaa ctttgcacat ggttaccca gcttttctgt 180
 atccattggt gttctttatc gaggcaagcc tgctgctgcc actgtggtgg aattttgtgg 240
 tgggcctatg tgctggagca ctggtacaat ttctgcatct tctggcaaag gtgcttattg 300
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 tggggtttgga tatgaacatg atgatgcatg gctcaccaat ataaatttgt tcaaggaatt 420
 tactgatgtt agcaggggag tacgaaggct aggctctgct gctgccgata tgtcccatgt 480
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 ttcaagaccc tttcactcaa ccggtatcgaa aattaaagcc gaactttaca taaaggagta 900
 gagctcgaat gagcttctca ctggattcct tttgctttga tcgaatgtat caggaagaaa 960
 tgtttgcaaa aggtgttgta tgcattggtt cagcctgttg tacttggaat aatataactg 1020
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aaaaaaaaaa

1090

<210> 10

<211> 249

<212> PRT

<213> Hordeum vulgare

<400> 10

His Glu Asp Lys Leu Ser Glu Ser Val Ile Leu Glu Val Val Thr Lys
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Asn Phe Arg Asp His Leu Ile Leu Gly Glu Glu Gly Gly Leu Ile Gly
20 25 30

Asp Ser Leu Ser Glu Tyr Leu Trp Cys Ile Asp Pro Leu Asp Gly Thr
35 40 45

Thr Asn Phe Ala His Gly Tyr Pro Ser Phe Ser Val Ser Ile Gly Val
50 55 60

Leu Tyr Arg Gly Lys Pro Ala Ala Ala Thr Val Val Glu Phe Cys Gly
65 70 75 80

Gly Pro Met Cys Trp Ser Thr Arg Thr Ile Ser Ala Ser Ser Gly Lys
85 90 95

Gly Ala Tyr Cys Asn Gly Gln Lys Ile His Val Ser Pro Thr Glu Lys
100 105 110

Val Glu Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp
115 120 125

Ala Trp Leu Thr Asn Ile Asn Leu Phe Lys Glu Phe Thr Asp Val Ser
130 135 140

Arg Gly Val Arg Arg Leu Gly Ser Ala Ala Ala Asp Met Ser His Val
145 150 155 160

Gly Leu Gly Ile Thr Glu Ala Tyr Trp Glu Tyr Arg Leu Lys Pro Trp
165 170 175

Asp Met Ala Ala Gly Val Leu Ile Val Glu Glu Ala Gly Gly Val Val
180 185 190

Thr Arg Met Asp Gly Gly Glu Phe Thr Val Phe Asp Arg Ser Val Leu
195 200 205

Val Ser Asn Gly Val Val His Asp Gln Leu Leu Glu Arg Ile Arg Pro
210 215 220

Ala Thr Glu Asp Leu Lys Lys Lys Gly Ile Asp Phe Ser Leu Trp Phe
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Lys Pro Asp Lys Tyr Pro Thr Asp Phe
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<210> 11

<211> 989

<212> DNA

<213> Zea mays

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agctcaaaaag tcagtcgggt acttgtcagg cttgaaccac aacgagaagt cgatcccttt 240
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ctaagaacaa aacctgtcca tgaacgccac aaacaatatg ccaaattgtt cacaacaaac 360
aaacctgtcc atgaacaagt ccgttggaag caagaacaga gcgatcgaag accgtaaact 420
ctccaccgtc catgcgagtt accaccccac cagcttcctc tactatcagg acgccagcat 480
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ccttgaacag attcatattg gtcgtccagg catcatcgtg ttcatatcca aaacctgtga 660
cgagaagtga ttgttccacc ttgtctgtct gactgacatg aatcctttgt ccaatataat 720
aagctcctcc gccagcaaat ggaaaaattg ttcggggtgg ccaacacata aggccgccac 780
aaaattctca cccacttgaa accacacggg ttttcccagg aaagaacaac taatggcaca 840
ggtaaaccgg ggggtaccat tggcaaaagt ccttgtctcc accaaagggt aattgcccc 900
aaggtctcct gaaaggggaat ctccaaaaag ggcgcctttt cccccaatt aaaggggggc 960
ttttaattct ttggggaaaa tctcaaaag 989

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<210> 12
<211> 136
<212> PRT
<213> Zea mays

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Tyr Tyr Ile Gly Gln Arg Ile His Val Ser Gln Thr Asp Lys Val Glu
          20              25              30

Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp Ala Trp
          35              40              45

Thr Thr Asn Met Asn Leu Phe Lys Glu Phe Thr Asp Ile Ser Arg Gly
          50              55              60

Val Arg Arg Leu Gly Ser Ala Ala Ala Asp Met Ser His Ile Gly Leu
          65              70              75              80

Gly Ile Thr Glu Ala Tyr Trp Glu Tyr Arg Leu Lys Pro Trp Asp Val
          85              90              95

His Ala Gly Val Leu Ile Val Glu Glu Ala Gly Gly Val Val Thr Arg
          100              105              110

Met Asp Gly Gly Glu Phe Thr Val Phe Asp Arg Ser Val Leu Val Ser
          115              120              125

Asn Gly Leu Val His Gly Gln Val
          130              135

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<210> 13
<211> 492
<212> DNA
<213> Zea mays

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<220>
<221> unsure
<222> (442)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (485)
<223> n = a, c, g or t

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cctcgccctcc gcaaacccta acccccgcgc tcgcctcctc cgcctccgcg ccgcctcgcc 180
cgtgtcggtcc gcggtcttga gcgcgagtg gcgccagccg atgagtacgg ttagggcctc 240
gttcgccgct ggggcggccg gccggagagc tgcggcagtg ggggagttgg cgacggagcg 300
gctggtggag gtggcgcaac gggcggcgga cgctgctggg gaggtgctca ngaagtactt 360
ccgccagcgg gttgagatca tcgacaaaga ggaccacagt cctgttataa ttgcagatag 420
aagaagcaga agaagcaatg gngtcagtta tactgaagag cttccctact caagccaatt 480
ttggngaaga ga 492

<210> 14
<211> 338
<212> PRT
<213> Zea mays

<400> 14
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Gly Leu Ala Ser Ala Asn Pro Asn Pro Arg Ser Arg Leu Leu Arg Leu
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Arg Ala Ala Ser Pro Val Ser Ser Ala Val Leu Ser Ala Ser Gly Arg
35 40 45
Gln Pro Met Ser Thr Val Arg Ala Ser Phe Ala Ala Gly Ala Ala Gly
50 55 60
Arg Arg Ala Ala Ala Val Gly Glu Leu Ala Thr Glu Arg Leu Val Glu
65 70 75 80
Val Ala Gln Arg Ala Ala Asp Ala Ala Gly Glu Val Leu Arg Lys Tyr
85 90 95
Phe Arg Gln Arg Val Glu Ile Ile Asp Lys Glu Asp His Ser Pro Val
100 105 110
Thr Ile Ala Asp Arg Glu Ala Glu Glu Ala Met Val Ser Val Ile Leu
115 120 125
Lys Ser Phe Pro Thr His Ala Ile Phe Gly Glu Glu Asn Gly Trp Arg
130 135 140
Cys Ala Glu Asn Ser Ala Asp Phe Val Trp Val Leu Asp Pro Ile Asp
145 150 155 160

Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Leu Phe Gly Thr Leu Ile
 165 170 175
 Ala Leu Leu His Asn Gly Lys Pro Val Ile Gly Val Ile Asp Gln Pro
 180 185 190
 Ile Leu Arg Glu Arg Trp Ile Gly Val Asp Gly Lys Gln Thr Thr Leu
 195 200 205
 Asn Gly Gln Glu Ile Ser Val Arg Ser Cys Asn Leu Leu Ala Gln Ala
 210 215 220
 Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Glu Ala Asp Ala Glu Asp
 225 230 235 240
 Ala Phe Ile Arg Val Arg Asn Lys Val Lys Val Pro Leu Tyr Gly Cys
 245 250 255
 Asp Cys Tyr Ala Tyr Ala Leu Leu Ala Ser Gly Phe Val Asp Ile Val
 260 265 270
 Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu Ser Leu Val Pro Val
 275 280 285
 Ile Glu Gly Ala Gly Gly Ser Ile Thr Asp Trp Arg Gly Asp Lys Leu
 290 295 300
 His Trp Pro Val Thr Ala Glu Ser Arg Pro Thr Ser Phe Asn Val Val
 305 310 315 320
 Ala Ala Gly Asp Ala Arg Val His Lys Glu Ala Leu Asp Ala Leu Arg
 325 330 335

Trp Arg

<210> 15
 <211> 593
 <212> DNA
 <213> *Oryza sativa*

<400> 15
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 acgaagacta ggttctgctg ctgctgacat gtcccacgtt gccctaggca ttacagaagc 180
 ctactgggaa taccgactta agccttgagg tatggctgct ggtgttctga tagttgaaga 240
 agctgggtgg atggtgtcac gcatggatgg tggggagttt accgtctttg atcgttctgt 300
 ccttgtttcc aatggtgttg tacatgatca gcttttggat cggattggcc ctgccacaga 360
 agatcttaag aagaaaggaa ttgatttctc cttgtggttt aaacccgaca aataccctac 420
 cgacttttaa gttgaactcc tcacccagag ctattttata ctactagaag aaaagagaaa 480
 aacagaggat cttatgttaa aatgccatgt acttgactga atatttggtt attgaagtcc 540
 tttgactcaa aaaaaaaaaa aaaaaaaaaa tcgagggggg gccggtacac aat 593

<210> 16
 <211> 142
 <212> PRT
 <213> *Oryza sativa*

<400> 16
 His Glu Leu Thr Lys Val Glu Gln Ser Leu Leu Val Thr Gly Phe Gly

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Tyr Glu His Asp Asp Ala Trp Val Thr Asn Ile Asn Leu Phe Lys Glu			
20	25	30	
Tyr Thr Asp Ile Ser Arg Gly Val Arg Arg Leu Gly Ser Ala Ala Ala			
35	40	45	
Asp Met Ser His Val Ala Leu Gly Ile Thr Glu Ala Tyr Trp Glu Tyr			
50	55	60	
Arg Leu Lys Pro Trp Asp Met Ala Ala Gly Val Leu Ile Val Glu Glu			
65	70	75	80
Ala Gly Gly Met Val Ser Arg Met Asp Gly Gly Glu Phe Thr Val Phe			
85	90	95	
Asp Arg Ser Val Leu Val Ser Asn Gly Val Val His Asp Gln Leu Leu			
100	105	110	
Asp Arg Ile Gly Pro Ala Thr Glu Asp Leu Lys Lys Lys Gly Ile Asp			
115	120	125	
Phe Ser Leu Trp Phe Lys Pro Asp Lys Tyr Pro Thr Asp Phe			
130	135	140	

<210> 17
 <211> 1103
 <212> DNA
 <213> Glycine max

<400> 17
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 tcggtaacaa agtcgccgat gctgccggag aagttatccg caaatacttc agaaaaaact 180
 tcgacgttat tcacaaacat gatctcagtc cagtaaccat tgcagatcaa tctgctgagg 240
 aggctatggg ttcaatcata ctagacaatt tcccttctca tgccatttac ggagaggaaa 300
 atgggtggag gtgtgaagaa aagaatgctg attatgtttg ggtattagat cccatagatg 360
 ggactaagag ctttattact gggaaaacctg tatttggtac tctcgttgct cttctacaaa 420
 atggcacacc aatccttggc ataattgatc aacctgtgtt aagagaaaagg tggatcggga 480
 tagcaggaaa gagaacctca ctgaacggag aagaaatata tacacgcact tgtgcggacc 540
 tttctcaagc atacctgtac accacaagcc cacatctgtt caatggagat gcagaagaag 600
 cattcattcg tgtagaagc aaggtaaaat tccaattgta tggctgcgac tgctatgcat 660
 atgcactttt gtcttctggg tttgtggatc ttgttgttga gtctggtctg aagccatacg 720
 attttcttgc attgattcct gttattgaag gcgctggagg tgtcataact gattggaaaag 780
 gagataaact gttttgggaa gcttctccac tttcaatcgc cacaagtgtt aatgttgtgg 840
 ctgctgggtga caaacagatt catcaacaag ctctagattc attgcagtgg aagtgatagc 900
 ttgaattaat cttcagtgca aataatcttc tctgcaaagt gtcttgattc agatgttcct 960
 aaggacatgt attaccgtac cattttcttg catttaagtt gaaaaccatg tactcagaat 1020
 cttgaataag ttctgcaga aattaacctc tttgtctatt gggttggtaaa aaaagggggg 1080
 gccgtacaaa tctccccgcc ccg 1103

<210> 18
 <211> 295
 <212> PRT
 <213> Glycine max

<400> 18
 Met Phe Ser Gln Cys His Phe Leu Ser His Ser Pro Ile Pro Asn Thr
 1 5 10 15


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<400> 19
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agcctcgccc tctgaggcgg ggggctgggc ggtggctgct gcgggtaagg aggggggtgga 180
catggagcgg ctgggtggcg tggcgagag cgcggcggat gcggcggggg aggtgctcag 240
gaagtacttc aggcagcgct tcgagatcat cgacaaagag gaccacagtc ccgtcacgat 300
cgctgataga gaagcagaag aagcaatgac ctcagtcata ctgaagagct ttcctactca 360
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35 40 45

Trp Ala Val Ala Ala Ala Gly Lys Glu Gly Val Asp Met Glu Arg Leu
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Val Ala Val Ala Gln Ser Ala Ala Asp Ala Ala Gly Glu Val Leu Arg
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Lys Tyr Phe Arg Gln Arg Phe Glu Ile Ile Asp Lys Glu Asp His Ser
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Pro Val Thr Ile Ala Asp Arg Glu Ala Glu Glu Ala Met Thr Ser Val
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Ile Leu Lys Ser Phe Pro Thr His Ala Val Phe Gly Glu Glu Asn Gly
115 120 125

Trp Arg Cys Ala Glu Lys Ser Ala Asp Tyr Val Trp Val Leu Asp Pro
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Ile Asp Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Leu Phe Gly Thr

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145 150 155 160
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 165 170 175
 Gln Pro Ile Leu Arg Glu Arg Trp Val Gly Val Asp Gly Lys Lys Thr
 180 185 190
 Thr Leu Asn Gly Gln Glu Ile Ser Val Arg Pro Cys Asn Val Leu Glu
 195 200 205
 Gln Ala Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Glu Gly Asp Ala
 210 215 220
 Glu Asp Ala Phe Ile Arg Val Arg Asp Lys Val Lys Val Pro Leu Tyr
 225 230 235 240
 Gly Cys Asp Cys Tyr Ala Tyr Ala Leu Leu Ala Ser Gly Phe Val Asp
 245 250 255
 Leu Val Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu Ser Leu Val
 260 265 270
 Pro Val Ile Glu Gly Ala Gly Gly Ser Ile Thr Asp Trp Glu Gly Asn
 275 280 285
 Lys Leu His Trp Pro Val Ser Ser Glu Ser Arg Pro Thr Ser Phe Asn
 290 295 300
 Val Val Ala Ala Gly Asp Ser His Val His Gly Gln Ala Leu Ala Ala
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 Leu Arg Trp Arg

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 <212> PRT
 <213> Lycopersicon esculentum

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 35 40 45
 Lys Ala Cys Glu Asp Leu Ile Phe Asn His Leu Lys Gln His Phe Pro
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 Ser His Lys Phe Ile Gly Glu Glu Thr Ser Ala Ala Thr Gly Asp Phe
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 Asp Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Val Asp Gly Thr
 85 90 95
 Thr Asn Phe Val His Gly Phe Pro Ser Val Cys Val Ser Ile Gly Leu

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Gly	Thr	Glu	Val	Gly	Thr	Thr	Arg	Asp	Asn	Leu	Thr	Val	Glu	Thr	Thr
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Thr	Arg	Arg	Ile	Asn	Asn	Leu	Leu	Phe	Lys	Val	Arg	Ser	Leu	Arg	Met
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Cys	Gly	Ser	Cys	Ala	Leu	Asp	Leu	Cys	Trp	Val	Ala	Cys	Gly	Arg	Leu
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Ser

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 <212> PRT
 <213> Lycopersicon esculentum

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 35 40 45
 Lys Ala Cys Glu Asp Phe Ile Phe Asn His Leu Lys Gln Arg Phe Pro
 50 55 60
 Ser His Lys Phe Ile Gly Glu Glu Thr Thr Ala Ala Cys Gly Asn Phe
 65 70 75 80
 Glu Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr
 85 90 95
 Thr Asn Phe Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu

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Thr	Ile	Glu	Lys	Lys	Pro	Thr	Val	Gly	Val	Val	Tyr	Asn	Pro	Ile	Ile			
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Asp	Glu	Leu	Phe	Thr	Gly	Ile	Asp	Gly	Lys	Gly	Ala	Phe	Leu	Asn	Gly			
	130					135					140							
Lys	Pro	Ile	Lys	Val	Ser	Ser	Gln	Ser	Glu	Leu	Val	Lys	Ala	Leu	Leu			
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Thr	Gly	Arg	Ile	Asn	Ser	Leu	Leu	Phe	Lys	Val	Arg	Ser	Leu	Arg	Met			
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Cys	Gly	Ser	Cys	Ala	Leu	Asn	Leu	Cys	Gly	Val	Ala	Cys	Gly	Arg	Leu			
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225					230					235					240			
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Phe	Ser	Leu	Trp	Gly	Lys	Val	Gln	Gln	Ile	Gln	Glu	Lys	Gly	Arg	Ala			
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Gly	Asp	Leu	Val	Thr	Glu	Ala	Asp	Arg	Gln	Ala	Glu	Ala	Ile	Ile	Leu			
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Glu	Ile	Ile	Lys	Arg	Arg	Cys	Pro	Asp	His	Ala	Ile	Leu	Ala	Glu	Glu			
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Ser	Gly	Gln	Leu	Gly	Gln	Val	Asp	Asn	Pro	Phe	Cys	Trp	Ala	Ile	Asp			
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Pro	Leu	Asp	Gly	Thr	Thr	Asn	Phe	Ala	His	Ser	Tyr	Pro	Val	Ser	Cys			
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Val	Ser	Ile	Gly	Leu	Leu	Ile	Gln	Asp	Ile	Pro	Thr	Val	Gly	Val	Val			

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Tyr	Asn	Pro	Phe	Arg	Gln	Glu	Leu	Phe	Arg	Ala	Ala	Thr	Ser	Leu	Gly
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Ala	Thr	Leu	Asn	Arg	Arg	Pro	Ile	Gln	Val	Ser	Thr	Thr	Ala	Ser	Leu
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Asp	Lys	Ser	Leu	Leu	Val	Thr	Gly	Phe	Ala	Tyr	Asp	Arg	Val	Lys	Thr
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Leu	Asp	Asn	Asn	Tyr	Pro	Glu	Phe	Cys	Tyr	Leu	Thr	His	Leu	Thr	Gln
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Cys	Gly	Arg	Leu	Asp	Gly	Tyr	Trp	Glu	Arg	Gly	Ile	Asn	Pro	Trp	Asp
210					215					220					
Met	Ala	Ala	Gly	Ile	Val	Ile	Val	Arg	Glu	Ala	Gly	Gly	Ile	Val	Ser
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Gln	Gly	Gly	Thr	Lys	Ile	Asp	Gln	Val	Ser	Ala	Ile	Val	Thr	Gln	Ala
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Ser	Gly	Tyr	Thr	Trp	Val	Leu	Asp	Pro	Ile	Asp	Gly	Thr	Ser	Ser	Phe
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Val	Arg	Gly	Leu	Pro	Ile	Phe	Ala	Thr	Leu	Ile	Gly	Leu	Val	Asp	Ala
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Ile	Val	Ser	Thr	Thr	Pro	Leu	Met	Phe	Thr	Thr	Pro	Val	Gln	Gln	Gln	
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Lys	Met	Ala	Asp	Ile	Tyr	Arg	Gln	Cys	Gln	Arg	Thr	Ala	Phe	Gly	Gly	
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225					230					235					240	
Lys	Glu	Leu	Thr	Pro	Glu	Ser	Thr	Glu	Val	Val	Ala	Ser	Pro	Asn	Pro	
				245					250					255		
Lys	Leu	His	Ser	Glu	Ile	Leu	Ala	Phe	Leu	Gln						
			260					265								